Assessment of the Geographic Origin of Romanian Common Bean Landraces

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The extreme weather that humanity has been confronting in recent years is the result of climate change. All over the world, unknown plant species are disappearing daily, which humankind has not discovered and will never know. Since 1900, the angiosperms and gymnosperms have been disappearing at a frequency of three species per year, but it is worrying that this rate of disappearance is up to 500 times higher currently. These data, correlated with the information provided by the United Nations (the world population will reach 10 billion by the year 2050) and FAO (food insecurity and the decrease of feedstock) lead to a crucial need to conserve and study plant germplasm. Therefore, plant germplasm conserved, especially in gene banks, can represent an important source for the development of varieties with an increased resistance to abiotic stress factors. Considering the origin of the current species of *Phaseolus vulgaris* L. as being in two distinct centres with different gene pools (Andean and Mesoamerica), the aim of the article is to infer the ancestry of 27 landraces according to their sampling geographical origin and morphological and molecular traits based on DNA sequences of three genes associated with abiotic stress tolerance (drought and thermal stress): *PvREB5A*, *PvDREB6B*, and *PvRPS4*. *Phaseolus vulgaris* L. has two different centres of origin: the Mesoamerican and the Andean basins. In this research, 27 landraces were evaluated from different counties in Romania. Three genes, *PvREB5A*, *PvDREB6B*, and *PvRPS4*, were amplified by the PCR reaction, sequenced by the Sanger technique, and the data obtained were analysed using MEGA XI software. For morphological data, the GraphPad Prism 9 software was used. According to *PvDREB5A*, 81.5% of all studied landraces belong to the Mesoamerican gene pool and 18.5% belong to the Andean. *PvDREB6B* revealed a high nucleotide and amino acid diversity between the Andean and Mesoamerican genotypes compared to the other evaluated genes. Also, the *PvRPS4* gene from the chloroplast genome showed one SNP within its coding region, different for those two gene pools, which is directly involved in a nonsynonymous substitution. The morphological characteristics, such as weight for 100 seeds, length, height, width, weight, seed flatness, flatness index, seed elongation, and eccentricity index were determined. European landraces of Mesoamerican origin indicated a large seed size compared to Andean genotypes. This work can be a foundation for the identification of interesting traits that establish plant adaptation to abiotic stress and conserve landraces of common beans from genetic depletion.

Keywords:

Phaseolus vulgaris L.; Mesoamerica; molecular and morphological traits; geographic origin; Andean

Reference: Galan, P.-M.; Leti, L.-I.; Strajeru, S.; Petrescu, D.-E.; Cimpeanu, M.-M.; Tanasa, A.-C.; Sandru, D.-M.; Gorgan, D.-L. Assessment of the Geographic Origin of Romanian Common Bean (*Phaseolus vulgaris* L.) Landraces Using Molecular Markers and Morphological Traits. *Agronomy* **2023**, *13*, 2820. https://doi.org/10.3390/agronomy13112820